**RAW SEQUENCE LISTING**
**PATENT APPLICATION: US/09/377,446**

DATE: 05/07/2001
TIME: 13:56:33

Input Set : **N:\Crf3\RULE60\09377446.txt**
Output Set: **N:\CRF3\05072001\I377446.raw**

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**ENTERED**

**SEQUENCE LISTING**
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 4 (1) GENERAL INFORMATION:
 6      (i) APPLICANT: Magal, Ella
 7                     Delaney, John M.
 9     (ii) TITLE OF INVENTION: METHOD FOR PREVENTING AND TREATING
10                             HEARING LOSS USING A NEURTURIN PROTEIN PRODUCT
12    (iii) NUMBER OF SEQUENCES: 5
14     (iv) CORRESPONDENCE ADDRESS:
15          (A) ADDRESSEE: Amgen Inc.
16          (B) STREET: One Amgen Center Drive
17          (C) CITY: Thousand Oaks
18          (D) STATE: California
19          (E) COUNTRY: USA
20          (F) ZIP: 91320-1789
22      (v) COMPUTER READABLE FORM:
23          (A) MEDIUM TYPE: Floppy disk
24          (B) COMPUTER: IBM PC compatible
25          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28     (vi) CURRENT APPLICATION DATA:
C--> 29     (A) APPLICATION NUMBER: US/09/377,446
C--> 30     (B) FILING DATE: 19-Aug-1999
31          (C) CLASSIFICATION:
33    (vii) PRIOR APPLICATION DATA:
34          (A) APPLICATION NUMBER: 09/106,486
35          (B) FILING DATE:
37   (viii) ATTORNEY/AGENT INFORMATION:
38          (A) NAME: Curry, Daniel R.
39          (B) REGISTRATION NUMBER: 32,727
40          (C) REFERENCE/DOCKET NUMBER: A-444
43 (2) INFORMATION FOR SEQ ID NO: 1:
45      (i) SEQUENCE CHARACTERISTICS:
46          (A) LENGTH: 102 amino acids
47          (B) TYPE: amino acid
48          (C) STRANDEDNESS: single
49          (D) TOPOLOGY: linear
51     (ii) MOLECULE TYPE: protein
56     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
58     Ala Arg Leu Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg
59      1               5                  10                  15
61     Val Ser Glu Leu Gly Leu Gly Tyr Ala Ser Asp Glu Thr Val Leu Phe
62                  20                  25                  30
64     Arg Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val Tyr Asp Leu
65                  35                  40                  45
67     Gly Leu Arg Arg Leu Arg Gln Arg Arg Arg Leu Arg Arg Glu Arg Val
68          50                  55                  60
70     Arg Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser
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Input Set : N:\Crf3\RULE60\09377446.txt
Output Set: N:\CRF3\05072001\I377446.raw

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 71        65                    70                   75                    80
 73·       Phe Leu Asp Ala His Ser Arg Tyr His Thr Val His Glu Leu Ser Ala
 74                          85                   90                    95
 76        Arg Glu Cys Ala Cys Val
 77                   100
 79 (2) INFORMATION FOR SEQ ID NO: 2:
 81        (i) SEQUENCE CHARACTERISTICS:
 82             (A) LENGTH: 100 amino acids
 83             (B) TYPE: amino acid
 84             (C) STRANDEDNESS: single
 85             (D) TOPOLOGY: linear
 87       (ii) MOLECULE TYPE: protein
 92       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 94        Pro Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser
 95        1               5                   10                  15
 97        Glu Leu Gly Leu Gly Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr
 98                     20                  25                  30
100        Cys Ala Gly Ala Cys Glu Ala Ala Ile Arg Ile Tyr Asp Leu Gly Leu
101                  35                  40                  45
103        Arg Arg Leu Arg Gln Arg Arg Arg Val Arg Arg Glu Arg Ala Arg Ala
104             50                  55                  60
106        His Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu
107        65                  70                  75                  80
109        Asp Val His Ser Arg Tyr His Thr Leu Gln Glu Leu Ser Ala Arg Glu
110                     85                  90                  95
112        Cys Ala Cys Val
113                   100
115 (2) INFORMATION FOR SEQ ID NO: 3:
117        (i) SEQUENCE CHARACTERISTICS:
118             (A) LENGTH: 312 base pairs
119             (B) TYPE: nucleic acid
120             (C) STRANDEDNESS: single
121             (D) TOPOLOGY: linear
123       (ii) MOLECULE TYPE: DNA (genomic)
126       (ix) FEATURE:
127             (A) NAME/KEY: CDS
128             (B) LOCATION: 1..309
131       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
133 ATG GCA CGT CTG GGT GCT CGT CCG TGT GGT CTG CGT GAA CTG GAA GTT      48
134 Met Ala Arg Leu Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val
135  1               5                   10                  15
137 CGT GTT TCC GAA CTG GGT CTG GGT TAC GCT TCC GAC GAA ACC GTT CTG      96
138 Arg Val Ser Glu Leu Gly Leu Gly Tyr Ala Ser Asp Glu Thr Val Leu
139              20                  25                  30
141 TTC CGT TAC TGT GCA GGT GCT TGT GAA GCA GCT GCA CGT GTT TAC GAC     144
142 Phe Arg Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val Tyr Asp
143          35                  40                  45
145 CTG GGT CTG CGT CGC CTG CGT CAG CGC CGT CGC CTG CGT CGC GAA CGT     192
146 Leu Gly Leu Arg Arg Leu Arg Gln Arg Arg Arg Leu Arg Arg Glu Arg
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147      50              55              60
149 GTT CGC GCA CAG CCG TGT TGC CGT CCG ACC GCA TAC GAA GAC GAA GTT     240
150 Val Arg Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val
151   65              70              75              80
153 TCC TTC CTG GAC GCT CAC TCC CGT TAC CAC ACC GTT CAC GAA CTG TCC     288
154 Ser Phe Leu Asp Ala His Ser Arg Tyr His Thr Val His Glu Leu Ser
155              85              90              95
157 GCA CGT CAC TGT GCG TGT GTT TAA                                     312
158 Ala Arg His Cys Ala Cys Val
159          100
162 (2) INFORMATION FOR SEQ ID NO: 4:
164      (i) SEQUENCE CHARACTERISTICS:
165          (A) LENGTH: 103 amino acids
166          (B) TYPE: amino acid
167          (D) TOPOLOGY: linear
169      (ii) MOLECULE TYPE: protein
171      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
173 Met Ala Arg Leu Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val
174   1              5              10              15
176 Arg Val Ser Glu Leu Gly Leu Gly Tyr Ala Ser Asp Glu Thr Val Leu
177              20              25              30
179 Phe Arg Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val Tyr Asp
180          35              40              45
182 Leu Gly Leu Arg Arg Leu Arg Gln Arg Arg Arg Leu Arg Arg Glu Arg
183   50              55              60
185 Val Arg Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val
186   65              70              75              80
188 Ser Phe Leu Asp Ala His Ser Arg Tyr His Thr Val His Glu Leu Ser
189              85              90              95
191 Ala Arg His Cys Ala Cys Val
192          100
194 (2) INFORMATION FOR SEQ ID NO: 5:
196      (i) SEQUENCE CHARACTERISTICS:
197          (A) LENGTH: 197 amino acids
198          (B) TYPE: amino acid
199          (C) STRANDEDNESS: single
200          (D) TOPOLOGY: linear
202      (ii) MOLECULE TYPE: protein
207      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
209      Met Gln Arg Trp Lys Ala Ala Ala Leu Ala Ser Val Leu Cys Ser Ser
210   1              5              10              15
212      Val Leu Ser Ile Trp Met Cys Arg Gln Gly Leu Leu Leu Ser His Arg
213              20              25              30
215      Leu Gly Pro Ala Leu Val Pro Leu His Arg Leu Pro Arg Thr Leu Asp
216          35              40              45
218      Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala
219          50              55              60
221      Pro Asp Ala Met Glu Leu Arg Glu Leu Thr Pro Trp Ala Gly Arg Pro
222   65              70              75              80
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